Amendments to the Claims:

The listing of claims provided below will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. (Currently amended) An isolated peptide comprising the peptide sequence of formula (I),

Xaa-Cys-Xab-Cys-Xac-Cys-Xad-Cys-Xae-Cys-Xaf-Cys-Xag (SEQ ID NO:39)

(I)

in which:

Xaa represents ~~is NH$_2$~~ an N-terminal NH$_2$- (amino) moiety or a ~~peptide residue~~ variable number of amino acid residues consisting essentially of from 1 to 10 ~~amino acids~~ residues; ~~preferably from 1 to 6 amino acids;~~

Xab ~~is a peptide residue~~ represents a variable number of amino acid residues consisting essentially of from 1 to 10 ~~amino acids~~ residues~~, preferably 10~~;

Xac ~~is a peptide residue of~~ represents 3 amino ~~acids~~ acid residues;

Xad represents the peptide sequence –Lys-Xad'-Xad"-Gly-His- (SEQ ID NO:40), in which Xad' represents 1 basic amino acid and Xad" represents a variable number of amino acid residues comprising from 0 to 5 residues ~~is a peptide residue consisting essentially of from 1 to 9 amino acids, preferably 9~~;

Xae ~~is a peptide residue~~ represents a variable number of amino acid residues consisting essentially of from 1 to 7 ~~amino acids~~ residues~~, preferably 7~~;

Xaf ~~is a peptide residue of~~ represents 1 amino acid residue; and

Xag ~~is —OH~~ represents a C-terminal –COOH (carboxyl) moiety or a ~~peptide residue~~ variable number of amino acid residues consisting essentially of from 1 to 5 ~~amino acids~~ residues~~, preferably 1 or 2 amino acids~~.

2. (Previously presented) The peptide of Claim 1, wherein

Xaa comprises at least one basic amino acid; and/or

Xad comprises at least one basic amino acid.

3. (Previously presented) The peptide of Claim 2, wherein Xad comprises 1, 2, 3 or 4 basic amino acids.

4. (Previously presented) The peptide of Claim 2, wherein the basic amino acids are selected from the group consisting of lysine, arginine and homoarginine.

5. (Cancelled).

6. (Previously presented) The peptide of Claim 1, wherein Xad represents the peptide sequence –Lys-Arg-Arg-Gly-Tyr-Lys-Gly-Gly-His- (SEQ ID NO:41).

7. (Previously presented) The peptide of Claim~~s~~ 1, wherein Xac comprises at least one acidic amino acid~~, preferably 1~~.

8. (Currently amended) The peptide of Claim 1, wherein Xac represents the peptide sequence -Asn-Xac'-Xac"-, in which Xac' represents ~~a peptide residue of~~ 1 amino acid, and Xac" represents ~~a peptide residue of~~ 1 acidic amino acid.

9. (Previously presented) The peptide of Claim 7, characterized in that the acidic amino acids are chosen from glutamic acid (Glu) or aspartic acid (Asp).

10. (Previously presented) The peptide of Claim 1, wherein Xac represents the peptide sequence –Asn-Gly-Glu-.

11. (Currently amended) The peptide of Claim 1, wherein Xaa represents the peptide sequence Xaa'-Gly-Xaa"- (SEQ ID NO:42), in which Xaa' represents ~~NH_2~~ an N-terminal NH_2-(amino) moiety or a ~~peptide residue~~ variable number of amino acid residues comprising 1 to 9 ~~amino acids~~ residues~~, preferably 1 to 5 amino acids~~, and Xaa" represents a ~~peptide residue~~ variable number of amino acid residues comprising at least one amino acid~~, preferably chosen from Leu, Ile, Val, Pro, Ser or Thr~~; and/or

Xab represents the peptide sequence –Val-Xab'-Asp- (SEQ ID NO:43) in which Xab' represents a ~~peptide residue~~ variable number of amino acid residues comprising from 0 to 8 ~~amino acids~~ residues~~, preferably 8~~; and/or

Xae represents the peptide sequence –Gly-Xae'-Asn- (SEQ ID NO:44), in which Xae' represents a ~~peptide residue~~ variable number of amino acid residues comprising from 0 to 5 ~~amino acids~~ residues~~, preferably 5~~; and/or

Xaf represents one of the amino acids Trp, Phe, Leu, Ile or Val; and/or

Xag represents the peptide sequence –Glu-Xag' (SEQ ID NO:45), in which Xag' represents ~~OH~~ a C-terminal –COOH (carboxyl) moiety or a variable number of amino acid residues ~~residue having a sequence~~ comprising from 1 to 4 ~~amino acids~~ residues~~, preferably 1 amino acid~~.

12. (Currently amended) The peptide of Claim 1, wherein Xaa represents the peptide sequence NH_2-Asp-Lys-Leu-Ile-Gly-Ser- (SEQ ID NO:46), in which NH_2- represents an N-terminal NH_2- (amino) moiety; and/or

Xab represents the peptide sequence –Val-Trp-Gly-Ala-Val-Asn-Tyr-Thr-Ser-Asp- (SEQ ID NO:47); and/or

Xae represents the peptide sequence -Gly-Ser-Phe-Ala-Asn-Val-Asn (SEQ ID NO:48); and/or

Xaf represents the amino acid -Trp-; and/or

Xag represents the peptide sequence –Glu-Thr-COOH, wherein -COOH represents a C-terminal carboxyl moiety.

13. (Previously presented) The peptide of Claim 1, wherein said peptide has the amino acid sequence encoded by SEQ ID NO:2.

14. (Currently amended) The peptide of Claim 1, wherein said peptide comprises at either of its ends, or at both ends, ~~peptide~~ amino acid residues necessary for its expression and ~~targeting~~ extracellular or subcellular localization in a host organism.

15. (Currently amended) The peptide of Claim 1, wherein the cysteine residues of the peptide of formula (I) form at least one intramolecular ~~disulphide~~ disulfide bridge.

16. (Previously presented) The peptide of Claim 15, wherein said peptide comprises disulfide bridges established between the first and fourth cysteine residues, the second and fifth cysteine residues, and the third and sixth cysteine residues of the peptide sequence of formula (I).

17. (Previously presented) A fusion peptide comprising the peptide of Claim 1.

18. (Previously presented) The fusion peptide of Claim 17, wherein the peptide comprises a signal peptide or a transit peptide.

19. (Currently amended) The fusion peptide of Claim 18, wherein the transit peptide is selected from the group consisting of the signal peptide ~~of~~ encoded by the tobacco PR-1α gene, the signal peptide present at the N-terminal of the precursor of factor Mat alpha 1, and the signal peptide ~~of~~ encoded by the maize polygalacturonase PG1 gene.

20. (Cancelled).

21. (Cancelled).

22. (Previously presented) A composition which comprises the peptide of Claim 1 and an appropriate vehicle.

23-45. (Cancelled).

46. (Previously presented) A method of preparing the peptide of Claim 1, comprising culturing a transformed organism that contains a nucleic acid encoding said peptide in an appropriate culture medium; extracting said peptide; and totally or partially purifying said peptide.

47. (New) The peptide of Claim 1, wherein Xaa represents an N-terminal NH_2- (amino) moiety or a variable number of amino acid residues consisting essentially of from 1 to 6 residues.

48. (New) The peptide of Claim 1, wherein Xab represents 10 amino acid residues.

49. (New) The peptide of Claim 1, wherein Xae represents 7 amino acid residues.

50. (New) The peptide of Claim 1, wherein Xag represents a C-terminal –COOH (carboxyl) moiety or a variable number of amino acid residues consisting essentially of from 1 to 2 amino acid residues.

51. (New) The peptide of Claim 1, wherein Xac comprises one acidic amino acid.

52. (New) The peptide of Claim 1, wherein Xaa represents the peptide sequence Xaa'-Gly-Xaa"- (SEQ ID NO:42), in which Xaa' represents an N-terminal NH_2- (amino) moiety or a variable number of amino acid residues comprising 1 to 5 residues, and Xaa" represents a variable number of amino acid residues comprising at least one amino acid selected from the group consisting of Leu, Ile, Val, Pro, Ser and Thr.

53. (New) The peptide of Claim 1, wherein Xab represents the peptide sequence –Val-Xab'-Asp- (SEQ ID NO:43) in which Xab' represents 8 amino acid residues.

54. (New) The peptide of Claim 1, wherein Xae represents the peptide sequence –Gly-Xae'-Asn- (SEQ ID NO:44), in which Xae' represents 5 amino acid residues.

55. (New) The peptide of Claim 1, wherein Xag represents the peptide sequence –Glu-Xag' (SEQ ID NO:45), in which Xag' represents a C-terminal –COOH (carboxyl) moiety or one amino acid residue.